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C¹
<120> ENDOGENETIC RETROVIRAL SEQUENCES, ASSOCIATED WITH AUTOIMMUNE DISEASES OR WITH PREGNANCY DISORDERS

<130> 105045

<140> US 09/446,024

<141> 1999-12-16

<150> PCT/FR98/01442

<151> 1998-07-06

<150> FR 97/08815

<151> 1997-07-07

<160> 53

<170> PatentIn version 3.1

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<223> n = any nucleotide

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<211> 22

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21

<210> 29

<211> 678

<212> DNA

<213> Artificial Sequence

<220>

<223> Ppol-MSRV probe

<220>

<221> misc_feature

<222> (594)..(594)

<223> n = any nucleotide

<400> 29
tcagggatag ccccatcta tttggccagg cattagccca agacttgagc cagttctcat 60
acctggatat tcttgtcctt tggatatgcg atgatttact tttagccgcc cgttcagaaa 120
ccttgtgcca tcaagccacc caagtgtctt taaatttctt cgccacctgt ggctacaagg 180
tttccaaacc aaaggctcag ctctgtctac agcagaaggc tatttaccct aaatacttag 240
ggctgaaatt atccaaaggc accagggccc tcagtgagga atgtatccag cctatactgg 300
cttatcctta tcccaaaacc ctaaaacaac taagaagggt ccttggcata ataggcataa 360
caggcataac aggttttctgc tgaatatgga ttcccaagta cggcaaaata gccagaccat 420
tatatacact aattaaggaa actcagaaag ccaataccca tttagtaaga tggacacctg 480
aagcagaggc agcttttcag gccgtaaaga acaccctaac ccaagcccca gtgttaagct 540
tgccagcggg gcaagacttt tctttctgtg tcacagaaaa aataggaata gctntagtag 600
tccttacaca ggtccgaggg accagcttgc aacccatggc atacctgagt aaggaaattg 660
atgtagtggc aaagggtt 678

<210> 30

<211> 536

<212> DNA

<213> Artificial Sequence

<220>

<223> Pgag-LB19 probe

<400> 30
ccaatctcca tgttgtatcc ccttcccca ctaataagga cccccctttc aacccaaaca 60
gtccaaaagg acatagacaa aggagtaaac aatgaaccaa agagtgccaa tattccctgg 120
ttatgcaccc tccaagcggg gggagaagaa ttcggcccag ccagagtgca tgtacctttt 180
tctctctcac acttgaagca aattaaaata gacctaggta aattctcaga tagccctgat 240
ggctatattg atgttttaca aggattagga caatcctttg atctgacatg gagagatata 300
atattactgc taaatcagac gctaacctca aatgagagaa gtgctgccat aactggagcc 360
cgagagtttg gcaatctctg gtatctcagt cagggtcaatg ataggatgac aacggaggaa 420
agagaacgat tccccacagg gcagcaggca gttcccagtg tagctcctca ttgggacaca 480

gaatcagaac atggagattg gtgccgcaga catttaaagc tttccccggg taccga 536

<210> 31

<211> 591

<212> DNA

<213> Artificial Sequence

<220>

<223> Penv-C15 probe

<400> 31

ccatggccat ctacactgaa caagatttat acaatcatgt cgtacctaaag cccacaaca 60
aaagagtacc cattcttctt tttgttatca gagcaggagt gctaggcaga ctaggtactg 120
gcattggcag tatcacaacc tctactcagt tctactacaa actatctcaa gaaataaatg 180
gtgacatgga acaggtcact gactccctgg tcaccttgca agatcaactt aactccctag 240
cagcagtagt ccttcaaaat cgaagagctt tagacttgct aaccgccaaa agagggggaa 300
cctgtttatt tttaggagaa gaacgctggt attatgttaa tcaatccaga attgtcactg 360
agaaagttaa agaaattcga gatcgaatac aatgtagagc agaggagctt caaacaccg 420
aacgctgggg cctcctcagc caatggatgc cctgggttct ccccttctta ggacctctag 480
cagctctaatt attgttactc ctctttggac cctgtatctt taacctcctt gttaagtttg 540
tctcttcag aattgaagct gttaaagctac agatggtctt acaaacttag a 591

<210> 32

<211> 364

<212> DNA

<213> Artificial Sequence

<220>

<223> Ppro-E probe

<400> 32

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tcacctcag agccccgggt atgtttgacc attgagagcc aggaagttaa ctgtctcctg 120

gacactggcg cagccttctc agtcttactt tctgtgccca gacaattgtc ctccagatct 180
 gtcactatcc gaggggtcct aggacagcca gtcactacat acttctctca gccactaagt 240
 tgtgactggg gaactttact cttttcacat gcttttctaa ttatgcctga aagccccact 300
 cccttgtag ggagagacat ttttagcaaaa gcagggggcca ttatacacct gaacaagctt 360
 gaaa 364

<210> 33

<211> 538

<212> PRT

<213> Human

<400> 33

Met Gly Leu Pro Tyr His Ile Phe Leu Cys Ser Val Leu Ser Pro Cys
 1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
 20 25 30

Pro His Pro Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
 50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
 65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
 100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
 115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Gly Val His Gly Thr Ser Ser
 130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Val Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Arg Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Glu Glu Ile Pro Asp Arg Ile Gln Arg Ile Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Arg Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asp Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 34

<211> 52

<212> PRT

<213> Human

<400> 34

Met Glu Pro Lys Met Gln Ser Lys Thr Lys Ile Tyr Arg Arg Pro Leu
 1 5 10 15

Asp Arg Pro Ala Ser Pro Arg Ser Asp Val Asn Asp Ile Lys Gly Thr
20 25 30

Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro Leu Leu Arg Pro Asn Ser
35 40 45

Ala Gly Ser Ser
50

<210> 35

<211> 48

<212> PRT

<213> Human

<400> 35

Met Leu Met Thr Ser Lys Ala Pro Leu Leu Arg Lys Ser Gln Leu His
1 5 10 15

Asn Leu Tyr Tyr Ala Pro Ile Gln Gln Glu Ala Val Arg Ala Val Val
20 25 30

Gly Gln Pro Pro Gln Gln His Leu Gly Phe Pro Val Glu Met Gly Asp
35 40 45

<210> 36

<211> 20

<212> DNA

<213> Human

<400> 36

atccaaagtg gtgagtaata

20

<210> 37

<211> 20

<212> DNA

<213> Human

<400> 37

cttttttcag atgggaaacg

20

<210> 38

<211> 10

<212> DNA

<213> Human

<400> 38

atccmaagtg

10

<210> 39

<211> 20

<212> DNA

<213> Human

<400> 39

caggaggaaa gtaactaaaa

20

<210> 40

<211> 10

<212> DNA

<213> Human

<400> 40

atgggaaacg

10

<210> 41

<211> 20

<212> DNA

<213> Human

<400> 41
ccatccctag atacatcctg 20

<210> 42

<211> 20

<212> DNA

<213> Human

<400> 42
tctcttccag aatcgaagct 20

<210> 43

<211> 873

<212> DNA

<213> Human

<400> 43
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ttgcaactga gagacaggac tagctggatt tcctaggccg actaagaatc cctaagccta 120
gctgggaagg tgaccacgtc cacctttaaa cacgggggctt gcaacttagc tcacacctga 180
ccaatcagag agctcactaa aatgctaatt aggcaaagac aggaggtaaa gaaatagcca 240
atcatctatt gcctgagagc acagcaggag ggacaacaat cgggatataa acccaggcat 300
tcgagctggc aacagcagcc cccctttggg tcccttcctt ttgtatggga gctgttttca 360
tgctatttca ctctattaaa tcttgcaact gcactcttct ggtccatggt tcttacggct 420
cgagctgagc ttttgctcac cgtccaccac tgctgtttgc caccaccgca gacctgccgc 480
tgactcccat ccctctggat cctgcagggt gtccgctgtg ctctgatcc agcgaggcgc 540
ccattgccgc tcccaattgg gctaaaggct tgccattggt cctgcacggc taagtgcctg 600
ggtttgttct aattgagctg aacactagtc actgggttcc atggttctct tctgtgacct 660
acggcttcta atagaactat aacacttacc acatggccca agattccatt ccttggaatc 720
cgtgaggcca agaactccag gtcagagaat acgaggcttg ccaccatctt ggaagcggcc 780
tgctaccatc ttggaagtgg ttcaccacca tcttgggagc tctgtgagca aggaccccc 840

ggtaacattt tggcaaccac gaacggacat cca

873

<210> 44

<211> 815

<212> DNA

<213> Human

<400> 44

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caggactagc tggatttcct aggctgacta agaatcccta agcctagctg ggaagggtgac	120
cacatccacc tttaaacacg gggcttgcaa cttagctcac acctgaccaa tcagagagct	180
cactaaaatg ctaattaggc aaagacagga ggtaaagaaa tagccaatca tctattgcct	240
gagagcacag caggagggtac aatgatcggg atataaaccc aagtcttcga gccggcaacg	300
gcaacccctt ttgggtcccc tccctttgta tgggagctct gttttcatgc tatttcactc	360
tattaaatct tgcaactgca ctcttctggt ccatgtttct tacggcttga gctgagcttt	420
cgctcgccat ccaccactgc tgtttgccgc caccgcagac ccgccgctga ctcccatccc	480
tctggatcat gcagggtgtc cgctgtgctc ctgatccagc gaggcacca ttgccgctcc	540
caatcgggct aaaggcttgc cattgttcct gcatggctaa gtgcctgggt tcatacctaat	600
tgagctgaac actagtcact gggttccatg gttctcttct gtgaccaca gcttctaata	660
gagctataac actcaccgca tggcccaagg ttccattcct tgaatccata aggccaagaa	720
ccccaggtca gagaacacga ggcttgccac catcttgga gctctgtgag caaggacccc	780
caagtaacac aaccatgagg gtgcaaatgc atggg	815

<210> 45

<211> 425

<212> DNA

<213> Human

<400> 45

caattcagca ggaagcagtt agagcgggtg tcggccaacc tccccaacag cacttaggtt	60
ttcctgttga gatgggggac tgagagacag gactagctgg atttcctagg ctgactaaga	120

atccttaagc ctaggtggga aggtgaccac atccaccttt aaacacgggg cttgcaactt	180
agctcacacc tgaccaatca gagagctcac taaaatgcta attaggcaaa gacaggaggt	240
aaagaaatag ccaatcattt attgcctgag agcacagcag gagggacaat gatcgggata	300
taaaccaag ttttcgagcc ggcaacggca accccctttg ggtcccctcc ctttgtatgg	360
gagctctggt ttcattgctat ttcactctat taaatcttgc aactgcaaaa aaaaaaaaaa	420
aaaaa	425

<210> 46

<211> 427

<212> DNA

<213> Human

<400> 46	
caattcagca ggaagcagtt agagcggtcg tcggccaacc tccccaacag cacttagggt	60
ttcctgttga gatgggggac tgagagacag gactagctgg atttcctagg ctgactaaga	120
atccctaagc ctagctggga aggtgaccac atccaccttt aaacacgggg cttgcaactt	180
agttcacacc tgaccaatca gagagctcac taaaatgcta attaggcaaa gacaggaggt	240
aaagaaatag ccaatcatct attgcatgag agcacagcag gagggacaat gatcgggata	300
taaaccaag tcttcgagcc ggcaacggca accccctttg ggtcccctcc ctttgtatgg	360
gagctctggt ttcattgctat ttcactctat taaatcttgc agctgcgaaa aaaaaaaaaa	420
aaaaaaa	427

<210> 47

<211> 600

<212> DNA

<213> Human

<400> 47	
caacaatcgg gatataaacc caggcattcg agctggcaac agcagcccc ctttgggtcc	60
cttccctttg tatgggagct gttttcatgc tatttcactc tattaaatct tgcaactgca	120
ctcttctggt ccatgtttct tacggctcga gctgagcttt tgctcaccgt ccaccactgc	180

tgtttgccac caccgcagac ctgccgctga ctcccatccc tctggatcct gcagggtgtc	240
cgctgtgctc ctgatccagc gaagcgccca ttgccgctcc caattgggct aaaggcttgc	300
cattgttcct gcacggctaa gtgcctgggt ttgttctaata tgagctgaac actagtcact	360
gggttccatg gttctcttct gtgaccacg gtttctaata gaactataac acttaccaca	420
tggccaaga ttccattcct tggaatccgt gaggccaaga actccaggtc agagaatacg	480
aagcttgcca ccatcttggg agcggcctgc taccatcttg gaagtgggtc accaccatct	540
tgggagctct gtgagcaagg accccccggt aacatttttg caaccacgaa cggacatcca	600

<210> 48

<211> 530

<212> DNA

<213> Human

<400> 48	
atgggagctg ttttcatgct atttcactct attaaatctt gcaactgcac tcttctggtc	60
catgtttctt acggctcgag ctgagctttt gctcaccgtc caccactgct gtttgccacc	120
accgcagacc tgccgctgac tcccatccct ctggatcctg cagggtgtcc gctgtgctcc	180
tgatccagcg aagcgcccat tgccgctccc aattgggcta aaggcttgcc attgttcctg	240
cacggctaag tgccctgggtt tgttctaatt gagctgaaca ctagtcactg ggttccatgg	300
ttctcttctg tgaccacagg cttctaataa aactataaca cttaccacat ggccaagat	360
tccattcctt ggaatccgtg aggccaacga actccaggtc agagaatacg aagcttgcca	420
ccatcttggg agcggcctgc taccatcttg gaagtgggtc accaccatct tgggagctct	480
gtgagcaagg accccccggt gacatttttg cgaccaccaa cggacatccc	530

<210> 49

<211> 486

<212> DNA

<213> Human

<220>

<221> misc_feature
 <222> (84)..(84)
 <223> n = any nucleotide

<220>

<221> misc_feature
 <222> (193)..(193)
 <223> n = any nucleotide

<220>

<221> misc_feature
 <222> (241)..(241)
 <223> n = any nucleotide

<400> 49
 actgcactct tctggtccat gtttcttacg gctcgagctg agcttttgct caccgtccac 60
 cactgctggt tgccaccacc gcanacctgc cgctgactcc catccctctg gatcctgcag 120
 ggtgtccgct gtgctcctga tccagcgagg cgccattgac cgctcccaat tgggctaaag 180
 gcttgccatt gtnccctgcac ggctaagtgc ctggggtttgt tctaattgag ctgaacacta 240
 ntcactgggt tccatgggtc tcttctgtga cccacgggctt ctaatagaac tataaacactt 300
 accacatggc ccaagattcc attccttgga atccgtgagg gcaagaactc caggtcagag 360
 aatacgaggc ttgccaccat cttggaagcg gcctgctacc atcttggaag tgggtcacca 420
 ccatcttggg agctctgtga gcaaggaccc cccggtaaca ttttggcaac cacgaacgga 480
 catcca 486

<210> 50

<211> 37

<212> PRT

<213> Human

<400> 50

Lys Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp
1 5 10 15

Val Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln
20 25 30

Pro Leu Leu Arg Pro
35

<210> 51

<211> 35

<212> PRT

<213> Human

<400> 51

Met Thr Ser Lys Ala Pro Leu Leu Arg Lys Ser Gln Leu His Asn Leu
1 5 10 15

Tyr Tyr Ala Pro Ile Gln Gln Glu Ala Val Arg Ala Val Val Gly Gln
20 25 30

Pro Pro Gln
35

<210> 52

<211> 33

<212> PRT

<213> Rex PTLV-L

<400> 52

Arg Leu Tyr Asn Thr Leu Ser Leu Asp Ser Pro Pro Ser Pro Pro Lys
1 5 10 15

Glu Leu Pro Ala Pro Ser Arg Phe Ser Pro Pro Gln Pro Leu Leu Arg
20 25 30

Pro

<210> 53

<211> 35

<212> PRT

<213> Tat SIV-AGM

<400> 53

Val	Thr	Tyr	His	Ala	Pro	Arg	Thr	Arg	Arg	Lys	Lys	Ile	Arg	Ser	Leu
1				5					10					15	

Asn	Leu	Ala	Pro	Leu	Gln	His	Gln	Ser	Ile	Ser	Thr	Lys	Trp	Gly	Arg
			20					25						30	

Asp	Gly	Gln
		35

C1
conc'd